



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

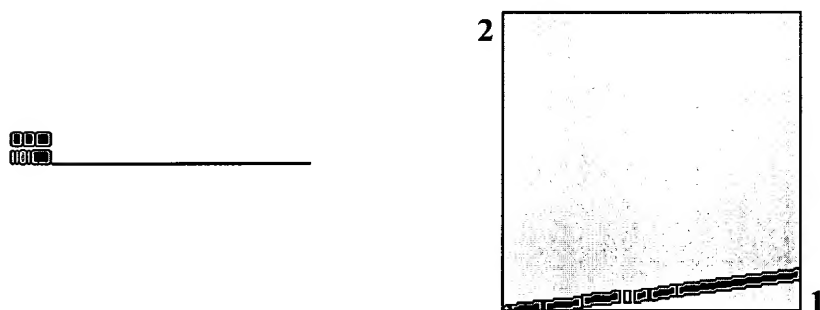
Matrix **BLOSUM62** gap open: **11** gap extension: **1**
 x_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☒ View option **Standard**
 Masking character option **X for protein, n for nucleotide** Masking color option **Black**
☐ Show CDS translation **Align**

Sequence 1: gi|47117817|sp|O75376|NCOR1_HUMAN Nuclear receptor corepressor 1 (N-CoR1) (N-CoR).

Length = 312 (1 .. 312) SEQ ID NO: 1

Sequence 2: gi|4559296|gb|AAD22972.1|AF125671.1 silencing mediator of retinoic acid and thyroid hormone receptor extended isoform [Mus musculus]

Length = 2462 (1 .. 2462)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.



Score = 200 bits (508), Expect = 1e-49

Identities = 179/315 (56%), Positives = 204/315 (64%), Gaps = 14/315 (4%)

Query	1	MSSSGYPPNQGA	FSTEQSRYP	PHSVQYTF	PNTRHQ	QEF	AVPDYR	SSHLE	VXXXXXXXXXX	60
		MS S P Q + +	RYPPH + Y		R + +	+Y+ H		S L		
Sbjct	1	MSGSTQPVAQ	-TWRAAEPR	YPHGISY	PVQIARS	HTDVGL	LLEYQ--	HHPRDY	TSHLSPGS	57
Query	61	XXXXXXXXXXXX	EFHGPS	DRPQER--	RTSYEP	FHPGPS	PVDHDS	LESKR	PRLEQVSDSH	118
		Q RRRPSLL	SEF PGS+R	QE R		F P	D +	ESKR	PRLE + D+	
Sbjct	58	IIQPQRRRPS	LLSEFQPG	SERSQEL	HLRPES	RTFLPE	LKGPDI	EFTES	KRPRLELLPDTL	117
Query	119	FQRVSA	AVLPLVH	PLPEGL	RASADAK	KDPAFG	GKHEAP	SSPISG	QPCGDDQNAS	PSKLSK 178
		+ L P G	S D KD +	GK E P	SP S		+ +PS+LSK			
Sbjct	118	LRPSPL---	LATGQPSG---	SEDLT	KDRSLAG	KLE-PV	SPSPPHAD	PELE	LAPSRLSK 169	
Query	179	EELIQS-MDR	VREIAX	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX						HRSIVQ 237

```
Sbjct 170 EELIQ+ +DRVDREI VEQQI KLKKKQQQLEEEAAKPPEPEKPVSPPP+E KHRS+VQ
EELIQNRLDRVDREITMVEQQISKLKKKQQQLEEEAAKPPEPEKPVSPPPIESKHRSVLVQ 229

Query 238 IIYDENRKKAEAAHKIFEGLGPKVELPLYNQPSDTKVYHENIKTNQVMRKKLILFFKRRN 297
IIYDENRKKAE AH+I EGLGP+VELPLYNQPSDT+ YHENIK NQ MRKKLIL+FKRRN
Sbjct 230 IIYDENRKKAEAAHRILEGLGPQVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRN 289

Query 298 HARKQREQKICQRYD 312
HARKQ EQ+ CQRYD
Sbjct 290 HARKQWEQRFCQRYD 304
```

CPU time: 0.04 user secs. 0.02 sys. secs 0.06 total secs.

Lambda K H
0.314 0.131 0.385

Gapped

Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1

Number of Hits to DB: 5554

Number of extensions: 3510

Number of successful extensions: 5

Number of sequences better than 10.0: 1

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 312

Length of database: 1,199,905,207

Length adjustment: 132

Effective length of query: 180

Effective length of database: 1,199,905,075

Effective search space: 215982913500

Effective search space used: 215982913500

Neighboring words threshold: 9

X1: 16 (7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 78 (34.7 bits)